SEQUENCE LISTING

<110> Potter, Andrew A.
Perez-Casal, Jose
Fontaine, Michael

<120> IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN AGAINST STREPTOCOCCUS INFECTION

<130> 9000-0057

<140> 09/878,766
<141> 2001-06-11

<160> 22

<170> PatentIn Ver. 2.0

<210> 1
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<400> 6
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<220>

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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer Gap-7

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<210> 10
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer Gap-8

<400> 10
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<210> 11
<211> 1011
<212> DNA
<213> Streptococcus dysgalactiae

<220>
<221> CDS
<222> (1)..(1011)

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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
1 5 10 15

gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tac gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

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aca act caa gga cgt ttt gac gga act gtt gaa gtt aaa gaa ggt gga   192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
     50                  55                  60

ttt gaa gta aac gga aac ttc atc aaa gtt tct gct gaa cgt gat cca   240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
 65                  70                  75                  80

gaa aac atc gac tgg gca act gac ggt gtt gaa atc gtt ctg gaa gca   288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
                 85                  90                  95

act ggt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct   336
Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
            100                 105                 110

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt   384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
        115                 120                 125

aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa   432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
    130                 135                 140

aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg   480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145                 150                 155                 160

gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act   528
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
                165                 170                 175

aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac   576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
            180                 185                 190

cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt   624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
        195                 200                 205

cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa   672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
    210                 215                 220

ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act   720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225                 230                 235                 240

gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt   768
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
                245                 250                 255
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gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt   816
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
            260                 265                 270

tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac   864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
        275                 280                 285

ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga   912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
    290                 295                 300

tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac   960
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

act gct caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa   1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
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taa                                                              1011
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<210> 12
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<212> PRT
<213> Streptococcus dysgalactiae

<400> 12

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  1               5                  10                  15

Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
            20                  25                  30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
        35                  40                  45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
    50                  55                  60

Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro
65                  70                  75                  80

Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
                85                  90                  95

Thr Gly Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
            100                 105                 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
        115                 120                 125
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Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
245 250 255

Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
290 295 300

Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305 310 315 320

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
325 330 335

<210> 13
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<212> DNA
<213> Streptococcus agalactiae

<220>
<221> CDS
<222> (1)..(1011)

<400> 13
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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
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gca ttc cgt cgc atc caa aac gta gaa ggt gtt gaa gtt act cgt atc    96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
             20                  25                  30

aac gac ctt aca gat cca aac atg ctt gca cac ttg ttg aaa tat gac   144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
         35                  40                  45

aca act caa ggt cgt ttc gac ggt act gtt gaa gtt aaa gaa ggt gga   192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
     50                  55                  60

ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca   240
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
 65                  70                  75                  80

gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca   288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
                 85                  90                  95

act ggt ttc ttt gca tca aaa gaa aaa gct gga caa cac atc cat gaa   336
Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
            100                 105                 110

aat ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt   384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
        115                 120                 125

aaa aca gtt gtt ttc aac act aac cac gat atc ctt gat gga act gaa   432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
    130                 135                 140

aca gtt atc tca ggt gct tca tgt act aca aac tgt ctt gct cca atg   480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145                 150                 155                 160

gct aaa gct tta caa gac aac ttt ggt gtt aaa caa ggt ttg atg act   528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
                165                 170                 175

act atc cac gca tac act ggt gac caa atg atc ctt gac gga cca cac   576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
            180                 185                 190

cgt ggt ggt gac ctt cgt cgt gct cgt gca ggt gct gca aac atc gtt   624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
        195                 200                 205

cct aac tca act ggt gct gca aaa gct atc gga ctt gtt atc cca gaa   672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
    210                 215                 220
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ttg aac ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act   720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225                 230                 235                 240

gga tca gta act gaa ttg gtt gca act ctt gaa aaa gac gta act gtc   768
Gly Ser Val Thr Glu Leu Val Ala Thr Leu Glu Lys Asp Val Thr Val
                245                 250                 255

gaa gaa gta aat gca gct atg aaa gca gca gct aac gat tca tac ggt   816
Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
            260                 265                 270

tat act gaa gat cca atc gta tca tct gat atc gtt ggt att tca tac   864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
        275                 280                 285

ggt tca ttg ttt gat gct act caa act aaa gtt caa act gtt gac ggt   912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
    290                 295                 300

aac caa ttg gtt aaa gtt gtt tca tgg tac gat aac gaa atg tca tac   960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

act tca caa ctt gtt cgt aca ctt gag tac ttt gca aaa atc gct aaa   1008
Thr Ser Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
                325                 330                 335

taa                                                              1011
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<210> 14
<211> 336
<212> PRT
<213> Streptococcus agalactiae

<400> 14

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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
            20                  25                  30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
        35                  40                  45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly
    50                  55                  60

Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65                  70                  75                  80
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Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

Thr Gly Phe Phe Ala Ser Lys Glu Lys Ala Gly Gln His Ile His Glu
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Thr Leu Glu Lys Asp Val Thr Val
245 250 255

Glu Glu Val Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305 310 315 320

Thr Ser Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
325 330 335

<210> 15
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<212> DNA
<213> Streptococcus uberis

<220>
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<222> (1)..(1011)

<400> 15

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  1               5                  10                  15

gca ttc cgt cgt att caa aac gtt gaa ggt gtt gaa gta act cgt att   96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
             20                  25                  30

aac gat ctt act gac cca aat atg ctt gca cac ttg ttg aaa tat gat   144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
         35                  40                  45

aca act caa ggt cgt ttc gac ggt aca gtt gaa gtt aaa gat ggt gga   192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
     50                  55                  60

ttc gaa gtt aac gga aac ttc atc aaa gtt tct gct gaa aaa gat cca   240
Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
 65                  70                  75                  80

gaa aac att gac tgg gca act gac ggt gta gaa atc gtt ctt gaa gca   288
Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
                 85                  90                  95

act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gct   336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala
            100                 105                 110

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga gat gat gtt   384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
        115                 120                 125

aaa act gtt gta ttt aac aca aac cat gac att ctt gac ggt aca gaa   432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
    130                 135                 140

act gta att tca ggt gct tca tgt act act aac tgt tta gct cca atg   480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145                 150                 155                 160

gct aaa gct ttg caa gat aac ttt ggt gtt aaa caa ggt ttg atg aca   528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
                165                 170                 175

act atc cac gct tac act ggt gac caa atg atc ctt gac gga cca cac   576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
            180                 185                 190
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cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gca agc aac att gtt   624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val
        195                 200                 205

cct aac tca act ggt gct gct aaa gca atc ggt ctt gta atc cca gaa   672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
    210                 215                 220

tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act   720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225                 230                 235                 240

gga tca gta act gaa tta gta gca gtt ctt gaa aaa gaa act tca gtt   768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val
                245                 250                 255

gaa gaa atc aac gca gca atg aaa gca gct gca aac gat tca tac gga   816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
            260                 265                 270

tac act gaa gac cca atc gta tct tct gat atc atc ggt atg gct tac   864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr
        275                 280                 285

ggt tca ttg ttt gat gct act caa act aaa gta caa act gtt gat gga   912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
    290                 295                 300

aat caa tta gtt aaa gtt gtt tca tgg tat gac aac gaa atg tct tac   960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

act gca caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa   1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
                325                 330                 335

taa                                                              1011
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<210> 16
<211> 336
<212> PRT
<213> Streptococcus uberis

<400> 16

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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
            20                  25                  30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
        35                  40                  45
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Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

Phe Glu Val Asn Gly Asn Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80

Glu Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Ala
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ser Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Glu Thr Ser Val
245 250 255

Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Ile Gly Met Ala Tyr
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305 310 315 320

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
325 330 335

<210> 17
<211> 1011
<212> DNA
<213> Streptococcus parauberis

<220>
<221> CDS
<222> (1)..(1011)

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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
1 5 10 15

gct ttc cgt cgt att caa aat gta gaa ggt gtt gaa gtt act cgc atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aac gac ctt aca gat cca aat atg ctt gca cac ttg tta aaa tac gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttt gac ggt act gta gaa gtt aaa gat ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

ttt gac gtt aac gga aaa ttc att aaa gtt tct gct gaa aaa gat cca 240
Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80

gaa caa att gac tgg gca act gac ggt gtt gaa atc gtt ctt gaa gca 288
Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

act ggt ttc ttt gct aaa aaa gca gct gct gaa aaa cat tta cat gaa 336
Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Glu
100 105 110

aat ggt gct aaa aaa gtt gtt atc act gct cct ggt gga gat gac gtg 384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125

aaa aca gtt gta ttt aac act aac cat gat atc ctt gat gga act gaa 432
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

aca gtt att tca ggt gct tca tgt act aca aac tgt tta gct cca atg 480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

gct aaa gct tta caa gat aac ttt ggc gta aaa caa ggt tta atg act 528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

```
aca atc cac gct tac act ggt gat caa atg ctt ctt gat gga cct cac   576
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His
            180                 185                 190

cgt ggt ggt gac tta cgt cgt gcc cgt gct ggt gct aac aat att gtt   624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val
        195                 200                 205

cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cct gaa   672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
    210                 215                 220

tta aat ggt aaa ctt gac ggt gct gca caa cgt gta cca gtt cca aca   720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225                 230                 235                 240

ggt tca gta aca gaa tta gta gca gtt ctt aat aaa gaa act tca gta   768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val
                245                 250                 255

gaa gaa att aac tca gta atg aaa gct gca gct aat gat tca tat ggt   816
Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
            260                 265                 270

tac act gaa gat cca atc gta tca tct gat atc gtt ggt atg tct ttc   864
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe
        275                 280                 285

ggt tca tta ttc gat gct act caa act aaa gta caa act gtt gat gga   912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
    290                 295                 300

aat caa tta gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac   960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

act gct caa ctt gat cgt aca ctt gag tac ttt gca aaa atc gct aaa  1008
Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
                325                 330                 335

taa                                                             1011
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<210> 18
<211> 336
<212> PRT
<213> Streptococcus parauberis

<400> 18
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Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
  1               5                  10                  15
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Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

Phe Asp Val Asn Gly Lys Phe Ile Lys Val Ser Ala Glu Lys Asp Pro
65 70 75 80

Glu Gln Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
85 90 95

Thr Gly Phe Phe Ala Lys Lys Ala Ala Ala Glu Lys His Leu His Glu
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asp Asp Val
115 120 125

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Leu Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Asn Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Val Leu Asn Lys Glu Thr Ser Val
245 250 255

Glu Glu Ile Asn Ser Val Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Met Ser Phe
275 280 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
290 295 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305 310 315 320

Thr Ala Gln Leu Asp Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
325 330 335

<210> 19
<211> 1011
<212> DNA
<213> Streptococcus iniae

<220>
<221> CDS
<222> (1)..(1011)

<400> 19
atg gta gtt aaa gtt ggt att aac ggt ttc gga cgt atc ggt cgt ctt 48
Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
1 5 10 15

gca ttc cgt cgt att caa aat gtt gaa ggt gtt gaa gta act cgt atc 96
Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

aat gac ctt aca gat cct aac atg ctt gca cac ttg ttg aaa tat gat 144
Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

aca act caa ggt cgt ttt gac ggt aca gtt gaa gtt aaa gat ggt gga 192
Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

ttc gaa gtt aac gga agc ttt gtt aaa gtt tct gca gaa cgc gaa cca 240
Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

gca aac att gac tgg gct act gat ggt gta gac atc gtt ctt gaa gca 288
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
85 90 95

aca ggt ttc ttc gct tct aaa gca gct gct gaa caa cac att cac gct 336
Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
100 105 110

aac ggt gcg aaa aaa gtt gtt atc aca gct cct ggt gga aat gac gtt 384
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

aaa aca gtt gtt tac aac act aac cat gat att ctt gat gga act gaa 432
Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

```
aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cca atg   480
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145                 150                 155                 160

gct aaa gca tta caa gat aac ttt ggt gta aaa caa ggt tta atg act   528
Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
                165                 170                 175

act atc cat ggt tac act ggt gac caa atg gtt ctt gac gga cca cac   576
Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
            180                 185                 190

cgt ggt ggt gat ctt cgt cgt gct cgt gca gct gca gca aac atc gtt   624
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Ala Asn Ile Val
        195                 200                 205

cct aac tca act ggt gct gct aaa gca atc ggt ctt gtt atc cca gaa   672
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
    210                 215                 220

tta aat ggt aaa ctt gac ggt gct gca caa cgt gtt cct gtt cca act   720
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225                 230                 235                 240

gga tca gta act gaa tta gta gca gtt ctt gaa aaa gat act tca gta   768
Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val
                245                 250                 255

gaa gaa atc aat gca gct atg aaa gca gca gct aac gat tca tac ggt   816
Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
            260                 265                 270

tac act gaa gat gct atc gta tca tca gat atc gta ggt att tct tac   864
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
        275                 280                 285

ggt tca tta ttt gat gct act caa act aaa gta caa act gtt gat gga   912
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
    290                 295                 300

aat caa ttg gtt aaa gtt gtt tca tgg tat gac aat gaa atg tct tac   960
Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

act gct caa ctt gtt cgt act ctt gag tac ttt gca aaa atc gct aaa   1008
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
                325                 330                 335

taa                                                              1011
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<210> 20
<211> 336

<212> PRT
<213> Streptococcus iniae

<400> 20

Met Val Val Lys Val Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu
1 5 10 15

Ala Phe Arg Arg Ile Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile
20 25 30

Asn Asp Leu Thr Asp Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp
35 40 45

Thr Thr Gln Gly Arg Phe Asp Gly Thr Val Glu Val Lys Asp Gly Gly
50 55 60

Phe Glu Val Asn Gly Ser Phe Val Lys Val Ser Ala Glu Arg Glu Pro
65 70 75 80

Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Asp Ile Val Leu Glu Ala
85 90 95

Thr Gly Phe Phe Ala Ser Lys Ala Ala Ala Glu Gln His Ile His Ala
100 105 110

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
115 120 125

Lys Thr Val Val Tyr Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
130 135 140

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
145 150 155 160

Ala Lys Ala Leu Gln Asp Asn Phe Gly Val Lys Gln Gly Leu Met Thr
165 170 175

Thr Ile His Gly Tyr Thr Gly Asp Gln Met Val Leu Asp Gly Pro His
180 185 190

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Ala Ala Ala Asn Ile Val
195 200 205

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
210 215 220

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
225 230 235 240

Gly Ser Val Thr Glu Leu Val Ala Val Leu Glu Lys Asp Thr Ser Val
245 250 255

Glu Glu Ile Asn Ala Ala Met Lys Ala Ala Ala Asn Asp Ser Tyr Gly
260 265 270

```
Tyr Thr Glu Asp Ala Ile Val Ser Ser Asp Ile Val Gly Ile Ser Tyr
        275                 280                 285

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Gln Thr Val Asp Gly
    290                 295                 300

Asn Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
305                 310                 315                 320

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
                325                 330                 335
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<210> 21
<211> 1347
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer Gap4
chimeric GapC protein

<220>
<221> CDS
<222> (1)..(1347)

<400> 21

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atg aaa aaa ata aca ggg att att tta ttg ctt ctt gca gtc att att   48
Met Lys Lys Ile Thr Gly Ile Ile Leu Leu Leu Leu Ala Val Ile Ile
  1               5                  10                  15

ctg tct gca tgc cag gca aac tac gga tcc ggt atg gta gtt aaa gtt   96
Leu Ser Ala Cys Gln Ala Asn Tyr Gly Ser Gly Met Val Val Lys Val
            20                  25                  30

ggt att aac ggt ttc ggt cgt atc gga cgt ctt gca ttc cgt cgt att   144
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala Phe Arg Arg Ile
        35                  40                  45

caa aat gtt gaa ggt gtt gaa gta act cgt atc aac gac ctt aca gat   192
Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn Asp Leu Thr Asp
    50                  55                  60

cca aac atg ctt gca cac ttg ttg aaa tac gat aca act caa gga cgt   240
Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp Thr Thr Gln Gly Arg
65                  70                  75                  80

ttt gac gga act gtt gaa gtt aaa gaa ggt gga ttt gaa gta aac gga   288
Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe Glu Val Asn Gly
                85                  90                  95

aac ttc atc aaa gtt tct gct gaa cgt gat cca gaa aac atc gac tgg   336
Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu Asn Ile Asp Trp
            100                 105                 110
```

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gca act gac ggt gtt gaa atc gtt ctg gaa gca ctc gag ggt act gta   384
Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Leu Glu Gly Thr Val
        115                 120                 125

gaa gtt aaa gat ggt gga ttt gac gtt aac gga aaa ttc att aaa gtt   432
Glu Val Lys Asp Gly Gly Phe Asp Val Asn Gly Lys Phe Ile Lys Val
    130                 135                 140

tct gct gaa aaa gat cca gaa caa att gac tgg gca act gac ggt gtt   480
Ser Ala Glu Lys Asp Pro Glu Gln Ile Asp Trp Ala Thr Asp Gly Val
145                 150                 155                 160

gaa atc gtt ctt gaa atc gat ggt act gtt gaa gtt aaa gaa ggt gga   528
Glu Ile Val Leu Glu Ile Asp Gly Thr Val Glu Val Lys Glu Gly Gly
                165                 170                 175

ttc gaa gtt aac ggt caa ttt gtt aaa gtt tct gct gaa cgc gaa cca   576
Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
            180                 185                 190

gca aac att gac tgg gct act gat ggc gta gaa atc gtt ctt gaa gca   624
Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
        195                 200                 205

act agt ttc ttt gct aaa aaa gaa gct gct gaa aaa cac tta cat gct   672
Thr Ser Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
    210                 215                 220

aac ggt gct aaa aaa gtt gtt atc aca gct cct ggt gga aac gac gtt   720
Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
225                 230                 235                 240

aaa aca gtt gtt ttc aac act aac cac gac att ctt gac ggt act gaa   768
Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
                245                 250                 255

aca gtt atc tca ggt gct tca tgt act aca aac tgt tta gct cct atg   816
Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
            260                 265                 270

gct aaa gct ctt cac gat gca ttt ggt atc caa aaa ggt ctt atg act   864
Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
        275                 280                 285

aca atc cac gct tat act ggt gac caa atg atc ctt gac gga cca cac   912
Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
    290                 295                 300

cgt ggt ggt gac ctt cgt cgt gct cgt gct ggt gct gca aac att gtt   960
Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
305                 310                 315                 320
```

```
cct aac tca act ggt gct gct aaa gct atc ggt ctt gtt atc cca gaa   1008
Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
                325                 330                 335

ttg aat ggt aaa ctt gat ggt gct gca caa cgt gtt cct gtt cca act   1056
Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
            340                 345                 350

gga tca gta act gag ttg gtt gta act ctt gat aaa aac gtt tct gtt   1104
Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
        355                 360                 365

gac gaa atc aac gct gct atg aaa gct gct tca aac gac agt ttc ggt   1152
Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
    370                 375                 380

tac act gaa gat cca att gtt tct tca gat atc gta ggc gtg tca tac   1200
Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
385                 390                 395                 400

ggt tca ttg ttt gac gca act caa act aaa gtt atg gaa gtt gac gga   1248
Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
                405                 410                 415

tca caa ttg gtt aaa gtt gta tca tgg tat gac aat gaa atg tct tac   1296
Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
            420                 425                 430

act gct caa ctt gtt cgt aca ctt gag tat ttt gca aaa atc gct aaa   1344
Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
        435                 440                 445

taa                                                              1347
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<210> 22
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GapC multiple epitope fusion protein

<400> 22

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Met Lys Lys Ile Thr Gly Ile Ile Leu Leu Leu Leu Ala Val Ile Ile
  1               5                  10                  15

Leu Ser Ala Cys Gln Ala Asn Tyr Gly Ser Gly Met Val Val Lys Val
            20                  25                  30

Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Leu Ala Phe Arg Arg Ile
        35                  40                  45
```

Gln Asn Val Glu Gly Val Glu Val Thr Arg Ile Asn Asp Leu Thr Asp
50 55 60

Pro Asn Met Leu Ala His Leu Leu Lys Tyr Asp Thr Thr Gln Gly Arg
65 70 75 80

Phe Asp Gly Thr Val Glu Val Lys Glu Gly Gly Phe Glu Val Asn Gly
85 90 95

Asn Phe Ile Lys Val Ser Ala Glu Arg Asp Pro Glu Asn Ile Asp Trp
100 105 110

Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala Leu Glu Gly Thr Val
115 120 125

Glu Val Lys Asp Gly Gly Phe Asp Val Asn Gly Lys Phe Ile Lys Val
130 135 140

Ser Ala Glu Lys Asp Pro Glu Gln Ile Asp Trp Ala Thr Asp Gly Val
145 150 155 160

Glu Ile Val Leu Glu Ile Asp Gly Thr Val Glu Val Lys Glu Gly Gly
165 170 175

Phe Glu Val Asn Gly Gln Phe Val Lys Val Ser Ala Glu Arg Glu Pro
180 185 190

Ala Asn Ile Asp Trp Ala Thr Asp Gly Val Glu Ile Val Leu Glu Ala
195 200 205

Thr Ser Phe Phe Ala Lys Lys Glu Ala Ala Glu Lys His Leu His Ala
210 215 220

Asn Gly Ala Lys Lys Val Val Ile Thr Ala Pro Gly Gly Asn Asp Val
225 230 235 240

Lys Thr Val Val Phe Asn Thr Asn His Asp Ile Leu Asp Gly Thr Glu
245 250 255

Thr Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met
260 265 270

Ala Lys Ala Leu His Asp Ala Phe Gly Ile Gln Lys Gly Leu Met Thr
275 280 285

Thr Ile His Ala Tyr Thr Gly Asp Gln Met Ile Leu Asp Gly Pro His
290 295 300

Arg Gly Gly Asp Leu Arg Arg Ala Arg Ala Gly Ala Ala Asn Ile Val
305 310 315 320

Pro Asn Ser Thr Gly Ala Ala Lys Ala Ile Gly Leu Val Ile Pro Glu
325 330 335

Leu Asn Gly Lys Leu Asp Gly Ala Ala Gln Arg Val Pro Val Pro Thr
340 345 350

Gly Ser Val Thr Glu Leu Val Val Thr Leu Asp Lys Asn Val Ser Val
355 360 365

Asp Glu Ile Asn Ala Ala Met Lys Ala Ala Ser Asn Asp Ser Phe Gly
370 375 380

Tyr Thr Glu Asp Pro Ile Val Ser Ser Asp Ile Val Gly Val Ser Tyr
385 390 395 400

Gly Ser Leu Phe Asp Ala Thr Gln Thr Lys Val Met Glu Val Asp Gly
405 410 415

Ser Gln Leu Val Lys Val Val Ser Trp Tyr Asp Asn Glu Met Ser Tyr
420 425 430

Thr Ala Gln Leu Val Arg Thr Leu Glu Tyr Phe Ala Lys Ile Ala Lys
435 440 445